IN THE CLAIMS:

Please amend claims 1-3 as shown in the following listing of the entire claims in the application.

1. (Currently Amended) An efficacy evaluation method of an interferon β treatment against multiple sclerosis, comprising the steps of:

labeling, with a fluorescent dye, a messenger RNA sample derived from peripheral blood leukocytes of a subject;

mixing and ~~thereby~~ hybridizing the fluorescence-labeled sample with different probes corresponding to at least one interferon induced protein gene, at least one interferon regulation factor gene, and at least one chemokine gene;

detecting fluorescence to ~~thereby~~ determine the expression levels of the at least one interferon induced protein gene, the at least one interferon regulation factor gene, and the at least one chemokine gene;

~~referring to~~ using a database comprising data on correlation between the ~~efficacy~~ clinical findings of an interferon β treatment against multiple sclerosis and the expression levels of the at least one interferon induced protein gene, the at least one interferon regulation factor gene, and the at least one chemokine gene; ~~and~~

~~evaluating~~ to evaluate the efficacy of the interferon β treatment against multiple sclerosis on the subject based on the measured gene expression levels and the correlation data.

2. (Currently Amended) The efficacy evaluation method according to claim 1, further comprising using at least one gene having a symbol name selected from the group consisting of IFIT1, IFIT4, G1P3, and ISG15 as the at least one interferon induced protein gene, using at least one gene having a symbol name selected from the group consisting of IRF1, IRF2, IRF3, IRF4, IRF5, IRF6, and IRF7 as the at least one interferon regulation factor gene, and using at least one gene having a symbol name selected from the group consisting of SCYA2, SCYA22, SCYA5, SCYB14, CCR5, CXCR3, CCR4, CCR3, CCR8, CXCR5, MIP-1α, MIG, IP-10, TARC, MDC, and SDF-1 as the at least one chemokine gene.

3. (Currently Amended) The efficacy evaluation method according to claim 2, further comprising using probes corresponding to at least one interleukin gene having a symbol name selected from the group consisting of IL4, IL10, IL12A, IL12B, and IL18, and to at least one transforming growth factor gene having a symbol name selected from the group consisting of TGFA, TGFB1, TGFB2, and TGFB3;

wherein the database further comprises data on correlation between the efficacy of the interferon β treatment and the expression levels of the at least one interleukin gene and the at least one transforming growth factor gene.

4. (Withdrawn) An oligonucleotide array for evaluating an interferon β treatment, comprising:

a substrate, and

probes immobilized on the substrate, the probes corresponding to at least one interferon induced protein gene, at least one interferon regulation factor gene, and at least one chemokine gene, all of which vary in their gene expression levels with the interferon β treatment.

5. (Withdrawn) The oligonucleotide array according to claim 4, wherein the at least one interferon induced protein gene is at least one gene having a symbol name selected from the group consisting of IFIT1, IFIT4, G1P3, and ISG15, wherein the at least one interferon regulation factor gene is at least one gene having a symbol name selected from the group consisting of IRF1, IRF2, IRF3, IRF4, IRF5, IRF6, and IRF7, and wherein the at least one chemokine gene is at least one gene having a symbol name selected from the group consisting of SCYA2, SCYA22, SCYA5, SCYB14, CCR5, CXCR3, CCR4, CCR3, CCR8, CXCR5, MIP-1α, MIG, IP-10, TARC, MDC, and SDF-1.

6. (Withdrawn) The oligonucleotide array according to claim 5, further comprising probes immobilized on the substrate, the probes corresponding to at least one interleukin gene having a symbol name selected from the group consisting of IL4, IL10, IL12A, IL12B, and IL18, and to at least one transforming growth factor gene having a symbol name selected from the group consisting of TGFA, TGFB1, TGFB2, and TGFB3.